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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/008,355

DATE: 12/18/2001

TIME: 16:23:46

Input Set : A:\23500440101.ST25.txt

Output Set: N:\CRF3\12182001\J008355.raw

ENTERED

3 <110> APPLICANT: Travis, James
 4 Potempa, Jan S
 5 Banbula, Agnieszka
 7 <120> TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use
 9 <130> FILE REFERENCE: 235.00440101
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/008,355
 C--> 11 <141> CURRENT FILING DATE: 2001-11-08
 11 <150> PRIOR APPLICATION NUMBER: US 60/246,827
 12 <151> PRIOR FILING DATE: 2000-11-08
 14 <160> NUMBER OF SEQ ID NOS: 26
 16 <170> SOFTWARE: PatentIn version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 2139
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Porphyromonas gingivalis
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 26 gtagccaaag cgcacaaagg catgtggtc ctcaacgaac tcaatcagga gaatctggat 120
 28 cgaatgcgtg agctcggctt tacgtcccg ttggattcgc tctacagttt cgacaagccg 180
 30 tccattgcca atgccgtggt tatcttcggt ggcggatgta ccggtatcac agtgtccgat 240
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 44 tttgctcctc ccagctctgt aggtaagtcc ggaggcgata cggacaactg gatgtggccg 660
 46 cgtcacacgg ggcacttcag cgtattccgc gtgtatgccg gtgccgacaa ccggccggcc 720
 48 gaatacagca aggacaataa accctataag cccgtttact tcgctgccgt atccatgcaa 780
 50 ggctacaagg ctgacgacta tgccatgacc atcggtttcc cgggcagtac ggatcgctac 840
 52 ctcaacttctt ggggtgtgga agatcgtatc gaaaacgaga acaatcctcg tatcgaagtt 900
 54 cgcggtatca agcaaggcat ctggaaggaa gccatgagcg cagatcaggc taccctgatac 960
 56 aaatatgcca gcaagtatgc tcagagtgtc aactattgga agaattcgat cggtatgaac 1020
 58 cgcggtctcg ctctcttga cgtgataggt cgtaagcgtg ccgaggaaag agcattcgca 1080
 60 gactggatcc gtaagaacgg caagagtgtc gtctatggcg atgtattgtc ttctctcgaa 1140
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 74 ctcaagtcca tggacaagga aaagtgtgac aaggctatcg agaaagatcc ggcagtagag 1560
 76 ctttccaaga gcgtaatagc tgctgctcgc gctattcagg ccgatgcgat ggccaatgcc 1620
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 84 aagcaggatc ctaagagcga tgagtttgcc gtacaggaga atatcctcga cctcttccgc 1860

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86 accaaaaaact atggctcgcta tgccgagaac ggtcagctcc atatcgcttt cctatcgaac 1920
88 aacgacatca cgggcggtaa ctccggtagc cccgtattcg ataagaacgg ccgtctgac 1980
90 ggtcttgctt tcgatggcaa ctgggaagct atgagtgggtg acatcgagtt cgaacccgat 2040
92 ctgcagcgca caatcagcgt ggacatccgc tacgtttctct tcatgattga caaatggggt 2100
94 cagtgcctccc gtctcatcca agagctgaag ttgatctaa 2139
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98 <211> LENGTH: 712
99 <212> TYPE: PRT
100 <213> ORGANISM: Porphyromonas gingivalis
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105 1 5 10 15
107 Gly Ala Ser Gly Val Ala Lys Ala Asp Lys Gly Met Trp Leu Leu Asn
108 20 25 30
110 Glu Leu Asn Gln Glu Asn Leu Asp Arg Met Arg Glu Leu Gly Phe Thr
111 35 40 45
113 Leu Pro Leu Asp Ser Leu Tyr Ser Phe Asp Lys Pro Ser Ile Ala Asn
114 50 55 60
116 Ala Val Val Ile Phe Gly Gly Gly Cys Thr Gly Ile Thr Val Ser Asp
117 65 70 75 80
119 Gln Gly Leu Ile Phe Thr Asn His His Cys Gly Tyr Gly Ala Ile Gln
120 85 90 95
122 Ser Gln Ser Thr Val Asp His Asp Tyr Leu Arg Asp Gly Phe Val Ser
123 100 105 110
125 Arg Thr Met Gly Glu Glu Leu Pro Ile Pro Gly Leu Ser Val Lys Tyr
126 115 120 125
128 Leu Arg Lys Ile Val Lys Val Thr Asp Lys Val Glu Gly Gln Leu Lys
129 130 135 140
131 Gly Ile Thr Asp Glu Met Glu Arg Leu Arg Lys Ala Gln Glu Val Cys
132 145 150 155 160
134 Gln Glu Leu Ala Lys Lys Glu Asn Ala Asp Glu Asn Gln Leu Cys Ile
135 165 170 175
137 Val Glu Pro Phe Tyr Ser Asn Asn Glu Tyr Phe Leu Ile Val Tyr Asp
138 180 185 190
140 Val Phe Lys Asp Val Arg Met Val Phe Ala Pro Pro Ser Ser Val Gly
141 195 200 205
143 Lys Phe Gly Gly Asp Thr Asp Asn Trp Met Trp Pro Arg His Thr Gly
144 210 215 220
146 Asp Phe Ser Val Phe Arg Val Tyr Ala Gly Ala Asp Asn Arg Pro Ala
147 225 230 235 240
149 Glu Tyr Ser Lys [Asp Asn Lys Pro Tyr Lys] Pro Val Tyr Phe Ala Ala
150 245 250 255
152 Val Ser Met Gln Gly Tyr Lys Ala Asp Asp Tyr Ala Met Thr Ile Gly
153 260 265 270
155 Phe Pro Gly Ser Thr Asp Arg Tyr Leu Thr Ser Trp Gly Val Glu Asp
156 275 280 285
158 Arg Ile Glu Asn Glu Asn Asn Pro Arg Ile Glu Val Arg Gly Ile Lys
159 290 295 300
161 Gln Gly Ile Trp Lys Glu Ala Met Ser Ala Asp Gln Ala Thr Arg Ile

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SID 19

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162 305 310 315 320
 164 Lys Tyr Ala Ser Lys Tyr Ala Gln Ser Ala Asn Tyr Trp Lys Asn Ser
 165 325 330 335
 167 Ile Gly Met Asn Arg Gly Leu Ala Arg Leu Asp Val Ile Gly Arg Lys
 168 340 345 350
 170 Arg Ala Glu Glu Arg Ala Phe Ala Asp Trp Ile Arg Lys Asn Gly Lys
 171 355 360 365
 173 Ser Ala Val Tyr Gly Asp Val Leu Ser Ser Leu Glu Lys Ala Tyr Lys
 174 370 375 380
 176 Glu Gly Ala Lys Ala Asn Arg Glu Met Thr Tyr Leu Ser Glu Thr Leu
 177 385 390 395 400
 179 Phe Gly Gly Thr Glu Val Val Arg Phe Ala Gln Phe Ala Asn Ala Leu
 180 405 410 415
 182 Ala Thr Asn Pro Asp Ala His Ala Gly Ile Leu Lys Ser Leu Asp Asp
 183 420 425 430
 185 Lys Tyr Lys Asp Tyr Leu Pro Ser Leu Asp Arg Lys Val Leu Pro Ala
 186 435 440 445
 188 Met Leu Asp Ile Val Arg Arg Arg Ile Pro Ala Asp Lys Leu Pro Asp
 189 450 455 460
 191 Ile Phe Lys Asn Val Ile Asp Lys Lys Phe Lys Gly Asp Thr Lys Lys
 192 465 470 475 480
 194 Tyr Ala Asp Phe Val Phe Asp Lys Ser Val Val Pro Tyr Ser Asp Lys
 195 485 490 495
 197 Phe His Ala Met Leu Lys Ser Met Asp Lys Glu Lys Phe Ala Lys Ala
 198 500 505 510
 200 Ile Glu Lys Asp Pro Ala Val Glu Leu Ser Lys Ser Val Ile Ala Ala
 201 515 520 525
 203 Ala Arg Ala Ile Gln Ala Asp Ala Met Ala Asn Ala Tyr Ala Ile Glu
 204 530 535 540
 206 Lys Gly Lys Arg Leu Phe Ala Gly Leu Arg Glu Met Tyr Pro Gly
 207 545 550 555 560
 209 Arg Ala Leu Pro Ser Asp Ala Asn Phe Thr Met Arg Met Ser Tyr Gly
 210 565 570 575
 212 Ser Ile Lys Gly Tyr Glu Pro Gln Asp Gly Ala Trp Tyr Asn Tyr His
 213 580 585 590
 215 Thr Thr Gly Lys Gly Val Leu Glu Lys Gln Asp Pro Lys Ser Asp Glu
 216 595 600 605
 218 Phe Ala Val Gln Glu Asn Ile Leu Asp Leu Phe Arg Thr Lys Asn Tyr
 219 610 615 620
 221 Gly Arg Tyr Ala Glu Asn Gly Gln Leu His Ile Ala Phe Leu Ser Asn
 222 625 630 635 640
 224 Asn Asp Ile Thr Gly Gly Asn Ser Gly Ser Pro Val Phe Asp Lys Asn
 225 645 650 655
 227 Gly Arg Leu Ile Gly Leu Ala Phe Asp Gly Asn Trp Glu Ala Met Ser
 228 660 665 670
 230 Gly Asp Ile Glu Phe Glu Pro Asp Leu Gln Arg Thr Ile Ser Val Asp
 231 675 680 685
 233 Ile Arg Tyr Val Leu Phe Met Ile Asp Lys Trp Gly Gln Cys Pro Arg
 234 690 695 700

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236 Leu Ile Gln Glu Leu Lys Leu Ile
237 705                      710
239 <210> SEQ ID NO: 3
240 <211> LENGTH: 52
241 <212> TYPE: PRT
242 <213> ORGANISM: Porphyromonas gingivalis
244 <400> SEQUENCE: 3
246 Thr Gly Gly Asn Ser Gly Ser Pro Val Phe Asp Lys Asn Gly Arg Leu
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249 Ile Gly Leu Ala Phe Asp Gly Asn Trp Glu Ala Met Ser Gly Asp Ile
250                      20                      25                      30
252 Glu Phe Glu Pro Asp Leu Gln Arg Thr Ile Ser Val Asp Ile Arg Tyr
253                      35                      40                      45
255 Val Leu Phe Met
256 50
258 <210> SEQ ID NO: 4
259 <211> LENGTH: 52
260 <212> TYPE: PRT
261 <213> ORGANISM: Staphylococcus aureus
263 <400> SEQUENCE: 4
265 Thr Gly Gly Asn Ser Gly Ser Pro Val Phe Asn Glu Lys Asn Glu Val
266 1                      5                      10                      15
268 Ile Gly Ile His Trp Gly Gly Val Pro Asn Glu Phe Asn Gly Ala Val
269                      20                      25                      30
271 Phe Ile Asn Glu Asn Val Arg Asn Phe Leu Lys Gln Asn Ile Glu Asp
272                      35                      40                      45
274 Ile His Phe Ala
275 50
277 <210> SEQ ID NO: 5
278 <211> LENGTH: 734
279 <212> TYPE: PRT
280 <213> ORGANISM: Shewanella putrefaciens
282 <400> SEQUENCE: 5
284 Met Ala Ser Gln Ala Leu Gly Phe Leu His Gln Asn Gly Leu Asn Thr
285 1                      5                      10                      15
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288                      20                      25                      30
290 His Ala Asp Glu Gly Met Trp Gln Pro His Gln Leu Pro Ala Met Ala
291                      35                      40                      45
293 Asp Val Leu Lys Ala Lys Gly Leu Glu Ile Asp Ala Lys Ser Ile Ser
294                      50                      55                      60
296 Lys Leu Thr Glu Phe Pro Met Asn Ala Val Ile Ser Leu Gly Gly Cys
297 65                      70                      75                      80
299 Thr Ala Ser Phe Val Ser Pro Lys Gly Leu Val Val Thr Asn His His
300                      85                      90                      95
302 Cys Ala Tyr Gly Ser Ile Gln Tyr Asn Ser Thr Pro Glu Lys Asn Leu
303                      100                     105                     110
305 Leu Gln Asp Gly Phe Leu Ala Lys Thr Phe Ala Asp Glu Leu Pro Ala
306                      115                     120                     125

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308 Ala Pro Gly Ser Arg Val Tyr Val Thr Glu Asp Val Thr Asn Val Thr
309      130                      135                      140
311 Glu Arg Val Lys Ala Gly Leu Glu Asn Lys Thr Gly Arg Glu Phe Tyr
312 145                      150                      155                      160
314 Gln Gly Val Glu Asn Gln Glu Lys Ala Leu Val Ala Glu Cys Glu Lys
315                      165                      170                      175
317 Asp Glu Gly Tyr Arg Cys Gln Val Tyr Ser Phe His Gly Gly Leu Glu
318                      180                      185                      190
320 Tyr Tyr Leu Val Lys Gln Leu Glu Ile Arg Asp Val Arg Leu Val Tyr
321                      195                      200                      205
323 Asn Pro Ala Gly Ser Val Gly Lys Tyr Gly Gly Asp Val Asp Asn Trp
324      210                      215                      220
326 Met Trp Pro Arg His Thr Gly Asp Tyr Ser Phe Tyr Arg Ala Tyr Val
327 225                      230                      235                      240
329 Ser Lys Asn Gly Lys Pro Ala Glu Phe Ser Ala Asp Asn Val Pro Tyr
330                      245                      250                      255
332 Glu Pro Lys Ser Phe Leu Lys Val Ser Ala Lys Gly Val Ser Glu Gly
333                      260                      265                      270
335 Asp Phe Val Met Val Ala Gly Tyr Pro Gly Arg Thr Asn Arg Tyr Arg
336                      275                      280                      285
338 Thr Ala Thr Glu Val Gln Asn Glu Phe Glu Trp Ala Tyr Pro Glu Gly
339      290                      295                      300
341 Lys Met Leu Arg Glu Arg Phe Ile Glu Ile Ile Lys Ala Thr Ala Pro
342 305                      310                      315                      320
344 Glu Gly Ser Asp Glu Arg Ile Lys Tyr Glu Ser Gln Ile Ala Gly Leu
345                      325                      330                      335
347 Ala Asn Tyr Ala Lys Asn Phe Thr Ser Met Ile Glu Phe Tyr Gly Lys
348                      340                      345                      350
350 Ser Thr Met Leu Ala Asp Arg Lys Ala Leu Glu Ala Lys Leu Ala Glu
351                      355                      360                      365
353 Trp Ile Ala Lys Asp Ser Ser Arg Glu Ala Lys Tyr Gly Lys Thr Leu
354      370                      375                      380
356 Ala Glu Leu Asp Ala Leu Ile Ala Lys Ser Lys Ala His Gln Glu Arg
357 385                      390                      395                      400
359 Asp Met Ile Leu Ser Tyr Ile Ser Ser Thr Thr Met Leu Pro Thr Ala
360                      405                      410                      415
362 Asn Asn Leu Tyr Arg Leu Ala His Glu Lys Gln Leu Pro Asp Met Gln
363                      420                      425                      430
365 Arg Glu Pro Gly Phe Gln Asp Arg Asp Met Thr Arg Phe Lys Ala Ser
366                      435                      440                      445
368 Met Glu Arg Ile Asp Arg Arg Tyr Ala Ala Ser Val Asp Lys Ala Val
369      450                      455                      460
371 Leu Phe Asp Met Leu Lys Arg Tyr Ala Ala Leu Pro Glu Ala Gln Arg
372 465                      470                      475                      480
374 Leu Pro Ala Met Asp Lys Ala Phe Gly Ile Asp Asn Lys Val Asn Glu
375                      485                      490                      495
377 Ala Lys Leu Ala Lys Thr Leu Asp Lys Met Tyr Ala Lys Thr Glu Leu
378                      500                      505                      510
380 Gly Asn Lys Asp Val Arg Leu Ala Trp Met Glu Lys Ser Val Asp Asp

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VERIFICATION SUMMARY

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Input Set : A:\23500440101.ST25.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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L:1006 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:1019 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
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